

## SEQUENCE LISTING

<110> Whitsett, Jeffrey  
Klaus H. Kaestner

<120> Diagnosis, prognosis and treatment of  
pulmonary diseases

<130> 10872/517745

<150> 60/519,453

<151> 2004-11-12

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aaaagagggt gggggtggg ggtgattgct ggtcgttgt tgtggctgt aaattttaaa 180  
ctgccatgca ctgcgctcc agt atg ctg gga gcg gtg aag atg gaa ggg cac 233  
Met Leu Gly Ala Val Lys Met Glu Gly His  
1 5 10

gag ccg tcc gac tgg agc agc tac tat gca gag ccc gag ggc tac tcc 281  
Glu Pro Ser Asp Trp Ser Ser Tyr Tyr Ala Glu Pro Glu Gly Tyr Ser  
15 20 25

tcc gtg agc aac atg aac gcc ggc ctg ggg atg aac ggc atg aac acg 329  
Ser Val Ser Asn Met Asn Ala Gly Leu Gly Met Asn Gly Met Asn Thr  
30 35 40

tac atg agc atg tcg gcg gcc gcc atg ggc agc ggc tcg ggc aac atg 377  
Tyr Met Ser Met Ser Ala Ala Ala Met Gly Ser Gly Ser Gly Asn Met  
45 50 55

agc gcg ggc tcc atg aac atg tcg tcg tac gtg ggc gct ggc atg agc 425  
Ser Ala Gly Ser Met Asn Met Ser Ser Tyr Val Gly Ala Gly Met Ser

60                    65                    70

ccg tcc ctg gcg ggg atg tcc ccc ggc gcg ggc gcc atg gcg ggc atg 473  
Pro Ser Leu Ala Gly Met Ser Pro Gly Ala Gly Ala Met Ala Gly Met  
75                    80                    85                    90

ggc ggc tcg gcc ggg gcg gcc ggc gtg gcg ggc atg ggg ccg cac ttg 521  
Gly Gly Ser Ala Gly Ala Ala Gly Val Ala Gly Met Gly Pro His Leu  
95                    100                    105

agt ccc agc ctg agc ccg ctc ggg ggg cag gcg gcc ggg gcc atg ggc 569  
Ser Pro Ser Leu Ser Pro Leu Gly Gly Gln Ala Ala Gly Ala Met Gly  
110                    115                    120

ggc ctg gcc ccc tac gcc aac atg aac tcc atg agc ccc atg tac ggg 617  
Gly Leu Ala Pro Tyr Ala Asn Met Asn Ser Met Ser Pro Met Tyr Gly  
125                    130                    135

cag gcg ggc ctg agc cgc gcc cgc gac ccc aag acc tac agg cgc agc 665  
Gln Ala Gly Leu Ser Arg Ala Arg Asp Pro Lys Thr Tyr Arg Arg Ser  
140                    145                    150

tac acg cac gca aag ccg ccc tac tcg tac atc tcg ctc atc acc atg 713  
Tyr Thr His Ala Lys Pro Pro Tyr Ser Tyr Ile Ser Leu Ile Thr Met  
155                    160                    165                    170

gcc atc cag cag agc ccc aac aag atg ctg acg ctg agc gag atc tac 761  
Ala Ile Gln Gln Ser Pro Asn Lys Met Leu Thr Leu Ser Glu Ile Tyr  
175                    180                    185

cag tgg atc atg gac ctc ttc ccc ttc tac cgg cag aac cag cag cgc 809  
Gln Trp Ile Met Asp Leu Phe Pro Phe Tyr Arg Gln Asn Gln Gln Arg  
190                    195                    200

tgg cag aac tcc atc cgc cac tcg ctc tcc ttc aac gac tgt ttc ctg 857  
Trp Gln Asn Ser Ile Arg His Ser Leu Ser Phe Asn Asp Cys Phe Leu  
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aag gtg ccc cgc tcg ccc gac aag ccc ggc aag ggc tcc ttc tgg acc 905  
Lys Val Pro Arg Ser Pro Asp Lys Pro Gly Lys Gly Ser Phe Trp Thr  
220                    225                    230

ctg cac cct gac tcg ggc aac atg ttc gag aac ggc tgc tac ctg cgc 953  
Leu His Pro Asp Ser Gly Asn Met Phe Glu Asn Gly Cys Tyr Leu Arg  
235                    240                    245                    250

cgc cag aag cgc ttc aag tgc gag aag cag ctg gcg ctg aag gag gcc 1001  
Arg Gln Lys Arg Phe Lys Cys Glu Lys Gln Leu Ala Leu Lys Glu Ala  
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gca ggc gcc gcc ggc agc ggc aag aag gcg gcc gcc gga gcc cag gcc 1049  
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gcg ggc acc gag tcg cct cac tcg agc gcc tcc ccg tgc cag gag cac 1145  
Ala Gly Thr Glu Ser Pro His Ser Ser Ala Ser Pro Cys Gln Glu His  
300 305 310

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Lys Arg Gly Gly Leu Gly Glu Leu Lys Gly Thr Pro Ala Ala Ala Leu  
315 320 325 330

agc ccc cca gag ccg gcg ccc tct ccc ggg cag cag cag cag gcc gcg 1241  
Ser Pro Pro Glu Pro Ala Pro Ser Pro Gly Gln Gln Gln Gln Ala Ala  
335 340 345

gcc cac ctg ctg ggc ccg ccc cac cac ccg ggc ctg ccg cct gag gcc 1289  
Ala His Leu Leu Gly Pro Pro His His Pro Gly Leu Pro Pro Glu Ala  
350 355 360

cac ctg aag ccg gaa cac cac tac gcc ttc aac cac ccg ttc tcc atc 1337  
His Leu Lys Pro Glu His His Tyr Ala Phe Asn His Pro Phe Ser Ile  
365 370 375

aac aac ctc atg tcc tcg gag cag cag cac cac cac agc cac cac cac 1385  
Asn Asn Leu Met Ser Ser Glu Gln Gln His His His Ser His His His  
380 385 390

cac caa ccc cac aaa atg gac ctc aag gcc tac gaa cag gtg atg cac 1433  
His Gln Pro His Lys Met Asp Ser Leu Lys Ala Tyr Glu Gln Val Met His  
395 400 405 410

tac ccc ggc tac ggt tcc ccc atg cct ggc agc ttg gcc atg ggc ccg 1481  
Tyr Pro Gly Tyr Gly Ser Pro Met Pro Gly Ser Leu Ala Met Gly Pro  
415 420 425

gtc acg aac aaa acg ggc ctg gac gcc tcg ccc ctg gcc gca gat acc 1529  
Val Thr Asn Lys Thr Gly Leu Asp Ala Ser Pro Leu Ala Ala Asp Thr  
430 435 440

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Ser Tyr Tyr Gln Gly Val Tyr Ser Arg Pro Ile Met Asn Ser Ser \*  
445 450 455

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35 40 45  
Ala Ala Met Gly Ser Gly Ser Gly Asn Met Ser Ala Gly Ser Met Asn  
50 55 60  
Met Ser Ser Tyr Val Gly Ala Gly Met Ser Pro Ser Leu Ala Gly Met  
65 70 75 80  
Ser Pro Gly Ala Gly Ala Met Ala Gly Met Gly Gly Ser Ala Gly Ala  
85 90 95  
Ala Gly Val Ala Gly Met Gly Pro His Leu Ser Pro Ser Leu Ser Pro  
100 105 110  
Leu Gly Gly Gln Ala Ala Gly Ala Met Gly Gly Leu Ala Pro Tyr Ala  
115 120 125  
Asn Met Asn Ser Met Ser Pro Met Tyr Gly Gln Ala Gly Leu Ser Arg  
130 135 140  
Ala Arg Asp Pro Lys Thr Tyr Arg Arg Ser Tyr Thr His Ala Lys Pro  
145 150 155 160  
Pro Tyr Ser Tyr Ile Ser Leu Ile Thr Met Ala Ile Gln Gln Ser Pro  
165 170 175  
Asn Lys Met Leu Thr Leu Ser Glu Ile Tyr Gln Trp Ile Met Asp Leu  
180 185 190  
Phe Pro Phe Tyr Arg Gln Asn Gln Gln Arg Trp Gln Asn Ser Ile Arg  
195 200 205  
His Ser Leu Ser Phe Asn Asp Cys Phe Leu Lys Val Pro Arg Ser Pro  
210 215 220  
Asp Lys Pro Gly Lys Gly Ser Phe Trp Thr Leu His Pro Asp Ser Gly  
225 230 235 240  
Asn Met Phe Glu Asn Gly Cys Tyr Leu Arg Arg Gln Lys Arg Phe Lys

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 Cys Glu Lys Gln Leu Ala Leu Lys Glu Ala Ala Gly Ala Ala Gly Ser  
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 Gly Lys Lys Ala Ala Ala Gly Ala Gln Ala Ser Gln Ala Gln Leu Gly  
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 Glu Ala Ala Gly Pro Ala Ser Glu Thr Pro Ala Gly Thr Glu Ser Pro  
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 His Ser Ser Ala Ser Pro Cys Gln Glu His Lys Arg Gly Gly Leu Gly  
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 Glu Leu Lys Gly Thr Pro Ala Ala Ala Leu Ser Pro Pro Glu Pro Ala  
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 Pro Ser Pro Gly Gln Gln Gln Gln Ala Ala Ala His Leu Leu Gly Pro  
 340            345            350  
 Pro His His Pro Gly Leu Pro Pro Glu Ala His Leu Lys Pro Glu His  
 355            360            365  
 His Tyr Ala Phe Asn His Pro Phe Ser Ile Asn Asn Leu Met Ser Ser  
 370            375            380  
 Glu Gln Gln His His His Ser His His His Gln Pro His Lys Met  
 385            390            395            400  
 Asp Leu Lys Ala Tyr Glu Gln Val Met His Tyr Pro Gly Tyr Gly Ser  
 405            410            415  
 Pro Met Pro Gly Ser Leu Ala Met Gly Pro Val Thr Asn Lys Thr Gly  
 420            425            430  
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cccgaggccg ttccgggtct gaactgtaac agggaggggc ctgcaggag cagcagcggg 180  
cgagtaaag t atg ctg gga gcg gtg aag atg gaa ggg cac gag ccg tcc 230  
Met Leu Gly Ala Val Lys Met Glu Gly His Glu Pro Ser  
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gac tgg agc agc tac tat gca gag ccc gag ggc tac tcc tcc gtg agc 278  
Asp Trp Ser Ser Tyr Tyr Ala Glu Pro Glu Gly Tyr Ser Ser Val Ser  
15 20 25

aac atg aac gcc ggc ctg ggg atg aac ggc atg aac acg tac atg agc 326  
Asn Met Asn Ala Gly Leu Gly Met Asn Gly Met Asn Thr Tyr Met Ser  
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atg tcg gcg gcc gcc atg ggc agc ggc tcg ggc aac atg agc gcg ggc 374  
Met Ser Ala Ala Ala Met Gly Ser Gly Ser Gly Asn Met Ser Ala Gly  
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Ser Met Asn Met Ser Ser Tyr Val Gly Ala Gly Met Ser Pro Ser Leu  
65 70 75

gcg ggg atg tcc ccc ggc gcg ggc gcc atg gcg ggc atg ggc ggc tcg 470  
Ala Gly Met Ser Pro Gly Ala Gly Ala Met Ala Gly Met Gly Gly Ser  
80 85 90

gcc ggg gcg gcc ggc gtg gcg ggc atg ggg ccg cac ttg agt ccc agc 518  
Ala Gly Ala Ala Gly Val Ala Gly Met Gly Pro His Leu Ser Pro Ser  
95 100 105

ctg agc ccg ctc ggg ggg cag gcg gcc ggg gcc atg ggc ggc ctg gcc 566  
Leu Ser Pro Leu Gly Gly Gln Ala Ala Gly Ala Met Gly Gly Leu Ala  
110 115 120 125

ccc tac gcc aac atg aac tcc atg agc ccc atg tac ggg cag gcg ggc 614  
Pro Tyr Ala Asn Met Asn Ser Met Ser Pro Met Tyr Gly Gln Ala Gly  
130 135 140

ctg agc cgc gcc cgc gac ccc aag acc tac agg cgc agc tac acg cac 662  
Leu Ser Arg Ala Arg Asp Pro Lys Thr Tyr Arg Arg Ser Tyr Thr His  
145 150 155

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Ala Lys Pro Pro Tyr Ser Tyr Ile Ser Leu Ile Thr Met Ala Ile Gln  
160 165 170

cag agc ccc aac aag atg ctg acg ctg agc gag atc tac cag tgg atc 758  
Gln Ser Pro Asn Lys Met Leu Thr Leu Ser Glu Ile Tyr Gln Trp Ile  
175 180 185

atg gac ctc ttc ccc ttc tac cgg cag aac cag cag cgc tgg cag aac 806  
Met Asp Leu Phe Pro Phe Tyr Arg Gln Asn Gln Gln Arg Trp Gln Asn  
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tcc atc cgc cac tcg ctc tcc ttc aac gac tgt ttc ctg aag gtg ccc 854  
Ser Ile Arg His Ser Leu Ser Phe Asn Asp Cys Phe Leu Lys Val Pro  
210 215 220

cgc tcg ccc gac aag ccc ggc aag ggc tcc ttc tgg acc ctg cac cct 902  
Arg Ser Pro Asp Lys Pro Gly Lys Gly Ser Phe Trp Thr Leu His Pro  
225 230 235

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Asp Ser Gly Asn Met Phe Glu Asn Gly Cys Tyr Leu Arg Arg Gln Lys  
240 245 250

cgc ttc aag tgc gag aag cag ctg gcg ctg aag gag gcc gca ggc gcc 998  
Arg Phe Lys Cys Glu Lys Gln Leu Ala Leu Lys Glu Ala Ala Gly Ala  
255 260 265

gcc ggc agc ggc aag aag gcg gcc gcc gga gcc cag gcc tca cag gct 1046  
Ala Gly Ser Gly Lys Lys Ala Ala Ala Gly Ala Gln Ala Ser Gln Ala  
270 275 280 285

caa ctc ggg gag gcc gcc ggg ccg gcc tcc gag act ccg gcg ggc acc 1094  
Gln Leu Gly Glu Ala Ala Gly Pro Ala Ser Glu Thr Pro Ala Gly Thr



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Gly Leu Gly Glu Leu Lys Gly Thr Pro Ala Ala Ala Leu Ser Pro Pro			
320 325 330			
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Glu Pro Ala Pro Ser Pro Gly Gln Gln Gln Ala Ala Ala His Leu			
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Leu Gly Pro Pro His His Pro Gly Leu Pro Pro Glu Ala His Leu Lys			
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ccg gaa cac cac tac gcc ttc aac cac ccg ttc tcc atc aac aac ctc	1334		
Pro Glu His His Tyr Ala Phe Asn His Pro Phe Ser Ile Asn Asn Leu			
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atg tcc tgc gag cag cag cac cac cac agc cac cac cac cca ccc	1382		
Met Ser Ser Glu Gln Gln His His His Ser His His His His Gln Pro			
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His Lys Met Asp Leu Lys Ala Tyr Glu Gln Val Met His Tyr Pro Gly			
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Tyr Gly Ser Pro Met Pro Gly Ser Leu Ala Met Gly Pro Val Thr Asn			
415 420 425			
aaa acg ggc ctg gac gcc tgc ccc ctg gcc gca gat acc tcc tac tac	1526		
Lys Thr Gly Leu Asp Ala Ser Pro Leu Ala Ala Asp Thr Ser Tyr Tyr			
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cag ggg gtg tac tcc ccg ccc att atg aac tcc tct taa gaagacgacg	1575		
Gln Gly Val Tyr Ser Arg Pro Ile Met Asn Ser Ser *			
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aaaaaaaaagt tatgtcataa aaatataaaa cgggtgctgtg actcacctgc tcttagccgc 180  
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ctatttct ctttcctag ccgcgagggt taaaccaatt atactgctt gtaacaaaag 720  
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cacacgaaat tgtggacacc tggatttggg ccaactattt cctattttct ccatctccta 360  
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cggcttgggt agctaacaat ataaatgaca tactctgttg tttcatgtt tgtttgttt 540  
ggggagacaa ggtttctctc ttagcccg atgtctgaa actcactcta tagactaggt 600  
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gccattatt gatttttt ctctgccct accccacct actgccctgt ttgtttagt 840  
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<211> 1002

<212> DNA

<213> homo sapiens

<220>

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<223> upstream promoter for FoxA1 from -1000 to 0

<400> 6

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<212> DNA

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<223> upstream promoter for FoxA2 from -1000 to 0

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